

#5

OIPE

## RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/834,792

TIME: 15:11:32

Input Set : A:\Figs1-5.txt

Output Set: N:\CRF3\12062001\I834792.raw

4 <110> APPLICANT: Mount Sinai School of Medicine of NYU  
 6 <120> TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL  
 7 CHANNEL EXPRESSED IN TASTE RECEPTOR CELL  
 10 <130> FILE REFERENCE: AP32911 070165.0589  
 12 <140> CURRENT APPLICATION NUMBER: 09/834,792  
 13 <141> CURRENT FILING DATE: 2001-04-13  
 15 <150> PRIOR APPLICATION NUMBER: 60/197,491  
 16 <151> PRIOR FILING DATE: 2000-04-17  
 18 <160> NUMBER OF SEQ ID NOS: 5  
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 4157  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Murine TRP8 cDNA  
 27 <400> SEQUENCE: 1

ENTERED

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29 agctcctgcc ccggcagccc cccagatact gaggatggct gggagcccat cctatgcagg 120
30 ggagagatca acttcggagg gtctgggaag aagcgaggca agtttgtaga ggtgccaagc 180
31 agtgtggccc cctctgtgct ttttgaactc ctgctcaccg agtggcacct gccagcccc 240
32 aacctggtgg gtccctggtt ggtgaggaa cgacctttgg ctatgaagtc gtggcttcgg 300
33 gatgtcctgc gcaaggggct ggtgaaagca gctcagagca cagggtgctg gatcctgacc 360
34 agtgccctcc acgtgggctt ggcccgccat gttggacaag ctgtacgtga tcaactctctg 420
35 gctagcacat ccaccaagat ccgtgtagt ggcacggaa tggcctctct ggatcgaatc 480
36 cttcacgctc aacttctaga tgggtgccac caaaaggagg ataactccat ccactaccca 540
37 gcagatgagg gcaacattca gggacccctc tgccccttgg acagcaatct ctcccacttc 600
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39 agcctggaga agcacatctc tcagcagagg acaggttatg ggggcaccag ctgcatccag 720
40 atacctgtcc tttgcctgtt ggtcaatggt gaccccaaca ccctagagag gatttccagg 780
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44 ttacagaaca ttgctgcaca cccccacctg ctacagtat atgacttcga gcaggagggg 1020
45 tcggaggacc tggacactgt catcctcaag gcacttgtga aagcctgcaa gagccacagc 1080
46 caagaagccc aagactacct agatgagctc aagttagcag tggcctggga tcgctgggac 1140
47 attgccaaga gtgaaatctt caatggggac gtggaatgga agtcctgtga cttggaagag 1200
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53 caggacgggc gcaggatgga ggagagagg ccacctaagc ggcccgcagg ccagaagtgg 1560
54 ctgccagacc tcagtaggaa gagtgaagac ccttgagggg acctgttctt ctgggctgtg 1620
55 ctgcagaatc gttatgagat ggccacatac ttctgggcca tgggcccggga ggggtgtggc 1680
56 gctgctctgg ctgcctgcaa gatcataaag gaaatgtccc acctggagaa agaggcagag 1740
57 gtggcccgcg ccatgctgta ggccaagtat gagcagctgg ccctggatct tttctcagag 1800
58 tgctacggca acagtgagga ccgtgccttt gccctgctgg tgcgaaggaa ccacagctgg 1860
59 agcaggacca cgtgcctgca cctggccact gaagctgatg ccaaggcctt ctttgcctat 1920

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60 gacgggtgtgc aagcattcct gaccaagatc tgggtggggag acatggccac aggcacaccc 1980
61 atcctacggc ttctgggtgc cttcacctgc ccagccctca tctacacaaa cctcatctcc 2040
62 ttcagtgagg atgccccgca gaggatggac ctagaagatc tgcaggagcc agacagcttg 2100
63 gatatggaaa agagcttcct atgcagccgg ggtggccaat tggagaagct aacagaggca 2160
64 ccaagggctc caggcgatct agggccacaa gctgccttcc tgctcacacg gtggaggaa 2220
65 ttctggggcg ctctgtgac tgtgttcctg gggaaatgtg tcatgtactt cgcattcctc 2280
66 ttctgtttca cctatgtcct gctgggtggac ttcaggccac caccacaggg gccgtctgga 2340
67 tccgaggtta ccctctatct ctgggtgttc aactgtgtgc tggaggaaat ccgacagggc 2400
68 ttcttcacag atgaggacac gcacctggtg aagaaattca ctctgtatgt ggaagacaac 2460
69 tggacaagt gtgacatggt ggccatcttc ctgttcattg tggagtcac ctgtagaatg 2520
70 gtgccctcgg tgtttgaggg tggcaggacc gttctggcca ttgacttcat ggtgttcaca 2580
71 cttcggtcca tccacatctt tgctattcac aagcagttgg gtcctaagat catcattgta 2640
72 gagcgaatga tgaaggatgt cttctttttc ctcttcttcc tgagcgtatg gcttgtggcc 2700
73 tatggtgtga ccactcaggg cctgctgcat ccccatgatg gccgtttgga gtggattttc 2760
74 cgccgtgtgc tatacagggc ttacctgcag atctttgggc aaatccctct ggatgaaatt 2820
75 gatgaggctc gtgtgaactg ttctcttcac cctctgctgc tggaaagctc ggcttcctgc 2880
76 cctaactctc atgccaactg gctggtcatt ctctgctgg ttaccttctc gcttgtcact 2940
77 aatgtgctgc tcatgaacct tctgatcgcc atgttcagct acacattcca ggtggtgcaa 3000
78 ggcaatgcag acatgtttct gaagtttcaa cgctaccacc tcatcgttga ataccatgga 3060
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82 gagaaacgga ggaggacag cgagggggag gtgctgagga aaacggcaca cagagtggac 3300
83 ttgattgcca aatacatcgg ggggctgaga gagcaagaaa agaggatcaa gtgtctggaa 3360
84 tcacaggcca actactgtat gctcctcttg tctctatga cggatacact ggctccagga 3420
85 ggcacctact caagctctca gaactgtggt tgcaggagtc agccagcctc tgctagagac 3480
86 agggagtacc tagagtctgg cttgccacc cttgacacct gaaatggaga aaccacttgc 3540
87 tctagagccc cagacctggc cacatcgagt ttttgggcca catcaacctt ccccaactcc 3600
88 cagcagcccc aagaaatggt cttcaaggcc ttgctacaga tcaactcttg gacatccctt 3660
89 cctaagagaa tgaactcat gtctttggca tctattcggg agcctcagaa gtatcctctc 3720
90 cagcagggca agatttttca tgtccacta aagctttcac tggcttgga tggacagctg 3780
91 gatctggcca agtctacat aggacaccat ctgcctggat ggggctatct aggtctaacc 3840
92 cctgtcttac cctgagttcc taagaagcca acctcttaaa cactaggttt ctttctgacc 3900
93 cctgaccac tcattagctg accagctcct agagggcagg actcagatct attgtaatta 3960
94 cctcccatct ttcaccccc acagcattat ctgtctgac attctggcag aaacccaag 4020
95 atattgctca aggtaccca atgctacttt actttctata aagcctgtag accacctcaa 4080
96 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4140
97 aaaaaaaaaa aaaaaaa 4157

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101 &lt;210&gt; SEQ ID NO: 2

102 &lt;211&gt; LENGTH: 1158

103 &lt;212&gt; TYPE: PRT

104 &lt;213&gt; ORGANISM: Murine TRP8

106 &lt;400&gt; SEQUENCE: 2

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107 Met Gln Thr Thr Ser Ser Cys Pro Gly Ser Pro Pro Asp Thr Glu
108 1 5 10 15
109 Asp Gly Trp Glu Pro Ile Leu Cys Arg Gly Glu Ile Asn Phe Gly Gly
110 20 25 30
111 Ser Gly Lys Lys Arg Gly Lys Phe Val Lys Val Pro Ser Ser Val Ala
112 35 40 45

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113 Pro Ser Val Leu Phe Glu Leu Leu Leu Thr Glu Trp His Leu Pro Ala
114      50              55              60
115 Pro Asn Leu Val Val Ser Leu Val Gly Glu Glu Arg Pro Leu Ala Met
116 65              70              75              80
117 Lys Ser Trp Leu Arg Asp Val Leu Arg Lys Gly Leu Val Lys Ala Ala
118      85              90              95
119 Gln Ser Thr Gly Ala Trp Ile Leu Thr Ser Ala Leu His Val Gly Leu
120      100             105             110
121 Ala Arg His Val Gly Gln Ala Val Arg Asp His Ser Leu Ala Ser Thr
122      115             120             125
123 Ser Thr Lys Ile Arg Val Val Ala Ile Gly Met Ala Ser Leu Asp Arg
124      130             135             140
125 Ile Leu His Arg Gln Leu Leu Asp Gly Val His Gln Lys Glu Asp Thr
126 145              150              155              160
127 Pro Ile His Tyr Pro Ala Asp Glu Gly Asn Ile Gln Gly Pro Leu Cys
128      165             170             175
129 Pro Leu Asp Ser Asn Leu Ser His Phe Ile Leu Val Glu Ser Gly Ala
130      180             185             190
131 Leu Gly Ser Gly Asn Asp Gly Leu Thr Glu Leu Gln Leu Ser Leu Glu
132      195             200             205
133 Lys His Ile Ser Gln Gln Arg Thr Gly Tyr Gly Gly Thr Ser Cys Ile
134      210             215             220
135 Gln Ile Pro Val Leu Cys Leu Leu Val Asn Gly Asp Pro Asn Thr Leu
136 225              230              235              240
137 Glu Arg Ile Ser Arg Ala Val Glu Gln Ala Ala Pro Trp Leu Ile Leu
138      245             250             255
139 Ala Gly Ser Gly Gly Ile Ala Asp Val Leu Ala Ala Leu Val Ser Gln
140      260             265             270
141 Pro His Leu Leu Val Pro Gln Val Ala Glu Lys Gln Phe Arg Glu Lys
142      275             280             285
143 Phe Pro Ser Glu Cys Phe Ser Trp Glu Ala Ile Val His Trp Thr Glu
144      290             295             300
145 Leu Leu Gln Asn Ile Ala Ala His Pro His Leu Leu Thr Val Tyr Asp
146 305              310              315              320
147 Phe Glu Gln Glu Gly Ser Glu Asp Leu Asp Thr Val Ile Leu Lys Ala
148      325             330             335
149 Leu Val Lys Ala Cys Lys Ser His Ser Gln Glu Ala Gln Asp Tyr Leu
150      340             345             350
151 Asp Glu Leu Lys Leu Ala Val Ala Trp Asp Arg Val Asp Ile Ala Lys
152      355             360             365
153 Ser Glu Ile Phe Asn Gly Asp Val Glu Trp Lys Ser Cys Asp Leu Glu
154      370             375             380
155 Glu Val Met Thr Asp Ala Leu Val Ser Asn Lys Pro Asp Phe Val Arg
156 385              390              395              400
157 Leu Phe Val Asp Ser Gly Ala Asp Met Ala Glu Phe Leu Thr Tyr Gly
158      405             410             415
159 Arg Leu Gln Gln Leu Tyr His Ser Val Ser Pro Lys Ser Leu Leu Phe
160      420             425             430
161 Glu Leu Leu Gln Arg Lys His Glu Glu Gly Arg Leu Thr Leu Ala Gly

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```

162          435          440          445
163 Leu Gly Ala Gln Gln Ala Arg Glu Leu Pro Ile Gly Leu Pro Ala Phe
164          450          455          460
165 Ser Leu His Glu Val Ser Arg Val Leu Lys Asp Phe Leu His Asp Ala
166 465          470          475          480
167 Cys Arg Gly Phe Tyr Gln Asp Gly Arg Arg Met Glu Glu Arg Gly Pro
168          485          490          495
169 Pro Lys Arg Pro Ala Gly Gln Lys Trp Leu Pro Asp Leu Ser Arg Lys
170          500          505          510
171 Ser Glu Asp Pro Trp Arg Asp Leu Phe Leu Trp Ala Val Leu Gln Asn
172          515          520          525
173 Arg Tyr Glu Met Ala Thr Tyr Phe Trp Ala Met Gly Arg Glu Gly Val
174          530          535          540
175 Ala Ala Ala Leu Ala Ala Cys Lys Ile Ile Lys Glu Met Ser His Leu
176 545          550          555          560
177 Glu Lys Glu Ala Glu Val Ala Arg Thr Met Arg Glu Ala Lys Tyr Glu
178          565          570          575
179 Gln Leu Ala Leu Asp Leu Phe Ser Glu Cys Tyr Gly Asn Ser Glu Asp
180          580          585          590
181 Arg Ala Phe Ala Leu Leu Val Arg Arg Asn His Ser Trp Ser Arg Thr
182          595          600          605
183 Thr Cys Leu His Leu Ala Thr Glu Ala Asp Ala Lys Ala Phe Phe Ala
184          610          615          620
185 His Asp Gly Val Gln Ala Phe Leu Thr Lys Ile Trp Trp Gly Asp Met
186 625          630          635          640
187 Ala Thr Gly Thr Pro Ile Leu Arg Leu Leu Gly Ala Phe Thr Cys Pro
188          645          650          655
189 Ala Leu Ile Tyr Thr Asn Leu Ile Ser Phe Ser Glu Asp Ala Pro Gln
190          660          665          670
191 Arg Met Asp Leu Glu Asp Leu Gln Glu Pro Asp Ser Leu Asp Met Glu
192          675          680          685
193 Lys Ser Phe Leu Cys Ser Arg Gly Gly Gln Leu Glu Lys Leu Thr Glu
194          690          695          700
195 Ala Pro Arg Ala Pro Gly Asp Leu Gly Pro Gln Ala Ala Phe Leu Leu
196 705          710          715          720
197 Thr Arg Trp Arg Lys Phe Trp Gly Ala Pro Val Thr Val Phe Leu Gly
198          725          730          735
199 Asn Val Val Met Tyr Phe Ala Phe Leu Phe Leu Phe Thr Tyr Val Leu
200          740          745          750
201 Leu Val Asp Phe Arg Pro Pro Pro Gln Gly Pro Ser Gly Ser Glu Val
202          755          760          765
203 Thr Leu Tyr Phe Trp Val Phe Thr Leu Val Leu Glu Ile Arg Gln
204          770          775          780
205 Gly Phe Phe Thr Asp Glu Asp Thr His Leu Val Lys Lys Phe Thr Leu
206 785          790          795          800
207 Tyr Val Glu Asp Asn Trp Asn Lys Cys Asp Met Val Ala Ile Phe Leu
208          805          810          815
209 Phe Ile Val Gly Val Thr Cys Arg Met Val Pro Ser Val Phe Glu Ala
210          820          825          830

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211 Gly Arg Thr Val Leu Ala Ile Asp Phe Met Val Phe Thr Leu Arg Leu
212      835      840      845
213 Ile His Ile Phe Ala Ile His Lys Gln Leu Gly Pro Lys Ile Ile Ile
214      850      855      860
215 Val Glu Arg Met Met Lys Asp Val Phe Phe Phe Leu Phe Phe Leu Ser
216 865      870      875      880
217 Val Trp Leu Val Ala Tyr Gly Val Thr Thr Gln Ala Leu Leu His Pro
218      885      890      895
219 His Asp Gly Arg Leu Glu Trp Ile Phe Arg Arg Val Leu Tyr Arg Pro
220      900      905      910
221 Tyr Leu Gln Ile Phe Gly Gln Ile Pro Leu Asp Glu Ile Asp Glu Ala
222      915      920      925
223 Arg Val Asn Cys Ser Leu His Pro Leu Leu Leu Glu Ser Ser Ala Ser
224      930      935      940
225 Cys Pro Asn Leu Tyr Ala Asn Trp Leu Val Ile Leu Leu Leu Val Thr
226 945      950      955      960
227 Phe Leu Leu Val Thr Asn Val Leu Leu Met Asn Leu Leu Ile Ala Met
228      965      970      975
229 Phe Ser Tyr Thr Phe Gln Val Val Gln Gly Asn Ala Asp Met Phe Trp
230      980      985      990
231 Lys Phe Gln Arg Tyr His Leu Ile Val Glu Tyr His Gly Arg Pro Ala
232      995      1000      1005
233 Leu Ala Pro Pro Phe Ile Leu Leu Ser His Leu Ser Leu Val Leu Lys
234      1010      1015      1020
235 Gln Val Phe Arg Lys Glu Ala Gln His Lys Arg Gln His Leu Glu Arg
236 1025      1030      1035      1040
237 Asp Leu Pro Asp Pro Leu Asp Gln Lys Ile Ile Thr Trp Glu Thr Val
238      1045      1050      1055
239 Gln Lys Glu Asn Phe Leu Ser Thr Met Glu Lys Arg Arg Arg Asp Ser
240      1060      1065      1070
241 Glu Gly Glu Val Leu Arg Lys Thr Ala His Arg Val Asp Leu Ile Ala
242      1075      1080      1085
243 Lys Tyr Ile Gly Gly Leu Arg Glu Gln Glu Lys Arg Ile Lys Cys Leu
244      1090      1095      1100
245 Glu Ser Gln Ala Asn Tyr Cys Met Leu Leu Leu Ser Ser Met Thr Asp
246 1105      1110      1115      1120
247 Thr Leu Ala Pro Gly Gly Thr Tyr Ser Ser Ser Gln Asn Cys Gly Cys
248      1125      1130      1135
249 Arg Ser Gln Pro Ala Ser Ala Arg Asp Arg Glu Tyr Leu Glu Ser Gly
250      1140      1145      1150
251 Leu Pro Pro Ser Asp Thr
252      1155
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258 <211> LENGTH: 3000
259 <212> TYPE: DNA
260 <213> ORGANISM: human
262 <400> SEQUENCE: 3
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VERIFICATION SUMMARY

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